

FIGURE 1

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SEQ ID NO:39  MYYHVRPKHAL-----FLAFYCYFS-----
SEQ ID NO:40  MKATLAAPSSLTSL-P-----YRTNSS-FGSKSSLFRSPSSSSSVS-MTTTRGNV
SEQ ID NO:38  MAN-----SXRPA-PLTPLHLRLDAAPPRPSLGHAAARPVPRVPLLPAR-XLRAPDGV
SEQ ID NO:28  MATVVRI-----PTISCIHIHTFRSQSPRTFARIRVGPWSWAPIRASA-ASSERGEI
SEQ ID NO:08  MATVVRI-----PTISCIHIHTFRSQSPRTFARIRVGPWSWAPIRASA-ASSERGEI
SEQ ID NO:22  MAHAALLHCSQSSR-SLAACRRGSHYRAPSH-VPRHSRRLRRRAVVSL--R-PMASSTA-
SEQ ID NO:24  AR--VQPTGALAPLHPLLRCTSRHLCASASPRAGLCLHHHRRRRSSRRRTKLAVRAMAPT
SEQ ID NO:26  FRH-----GH-----AL-----
1
60

SEQ ID NO:39  LLTMASATIASADLYEKIKNFYDDSSGLWEDVWGEHMHGYYGPHGTYRI---DRRQAQI
SEQ ID NO:40  AVAAAAATSTEALRKGIAEFYNETSGLWEIWDHMHGIFYDPDSSVQLSDSGHKEAQI
SEQ ID NO:38  VDRGPGDAAPPGLKEGIAGLYDESSGLWESIWEHMHGIFYDSGEAASMSD--HRRAQI
SEQ ID NO:28  VLEQPKKDDKKLQKGIAEFYDESSGLWENIWDHMHGIFYDSDTVSLSD--HRAAQI
SEQ ID NO:08  VLEQPKKDDKKLQKGIAEFYDESSGLWENIWDHMHGIFYDSDTVSLSD--HRAAQI
SEQ ID NO:22  ---QAPATAAPPGLKEGIAGLYDESSGLWENIWDHMHGIFYDSSEAAASMD--HRRAQI
SEQ ID NO:24  LSSSTAAAAPPGLKEGIAGLYDESSGVWESIWEHMHGIFYDAGEAASMSD--HRRAQI
SEQ ID NO:26  -----
61
120

SEQ ID NO:39  DLIKELLAWAVPQNSA----KPRKILDGCGIGGSSSLYLAQQHQAQAEVMGASLSPQVERA
SEQ ID NO:40  RMIEESLRFAGVTDEEE-EKKIKKVVDVCGGIGGSSRYLASKFGAECIGITLSPVQAKRA
SEQ ID NO:38  RMIEEALAFAAVP--DDPTNKPTIVDVCGGIGGSSRYLANKYGAQCSGITLSPVQAERG
SEQ ID NO:28  RMIQESLRFASV--SEERSKWPKSIVDVCGGIGGSSRYLAKKFGATSVGITLSPVQAQRA
SEQ ID NO:08  RMIQESLRFASV--SEERSKWPKSIVDVCGGIGGSSRYLAKKFGATSVGITLSPVQAQRA
SEQ ID NO:22  RMIEEALAFAGVPASDDPEKTPKTIVDVCGGIGGSSRYLAKKYGXQCTGITLSPVQAERG
SEQ ID NO:24  RMIEESLAF-----
SEQ ID NO:26  -----
121
180

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## FIGURE 1

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SEQ ID NO:39  GERARALGLGSTCQFQVANALDLPFASDSFDWVWSLESGEHMPNKAQFLQEAWRVLKPGG
SEQ ID NO:40  NDIAAAQSLSHKASFQVADALDQPFEDGKFDLVWSMESGEHMPDKAKFVKELVRVAAPGG
SEQ ID NO:38  NALAAAQGLSDKASFQVADALEQPFDPGQFDLVWSMESGEHMPNKKFVSELARVAAPGA
SEQ ID NO:28  NALAAAQGLADKVSFQVADALQQPFSDGQFDLVWSMESGEHMPDKAKFVGELARVAAPGA
SEQ ID NO:08  NALAAAQGLADKVSFQVADALQQPFSDGQFDLVWSMESGEHMPDKAKFVGELARVAAPGA
SEQ ID NO:22  NALAAAQGLSDQVTLQVADALEQPFDPGQFDLVWSMESGEHMPDKRKFVSELARVAAPGG
SEQ ID NO:24  -----
SEQ ID NO:26  -----AQPFDPGQFDLVWSMESDEHMPDKRQFVSELARVAAPGA
                                     181      240

SEQ ID NO:39  RLILATWCHRPIDPGNGPLTADERRHLQAIYDVYCLPYVVSPLPDYEAIARECGFGEIKTA
SEQ ID NO:40  RIIIVTWCHRNLSAGEEALQPEQNILDKICKTFYLPWCSTDDYVNLQSHSLQDIKCA
SEQ ID NO:38  TIIIVTWCHRNLPSEDSLKPDELNLLKKICDAYYLPDWCSPSDYVVKIAESLSLEDIKTA
SEQ ID NO:28  IIIIVTWCHRDLPDEQSLHPWEQDLLKKICDAYYLPWCSTSDYVKKLQSLQSLQDIKSE
SEQ ID NO:08  IIIIVTWCHRDLPDEQSLHPWEQDLLKKICDAYYLPWCSTSDYVKKLQSLQSLQDIKSE
SEQ ID NO:22  TIIIVTWCHRNLDPSETSLKPDELNLLRRICDAYYLPDWCSPSDYVVKIAESLSLEDIKTA
SEQ ID NO:24  -----
SEQ ID NO:26  RIIIVTWCHRNLEPSEESLKPDELNLLKRICDAYYLPDWCSPSDYVVKIAESLSLEDIRTA
                                     241      300

SEQ ID NO:39  DWSVAVAPFWDRVIESAFDPRVLWALGQAGPKIINAAALCLRLMKWYERGLVRFGLLTGI
SEQ ID NO:40  DWSENVAPFWPAAVIRTALTWKGLVSLRSGMKSIKGALTMPLMIEGYKKGVIKFGIITCQ
SEQ ID NO:38  DWSENVAPFWPAAVQSALTWKGLTSLRSGWKTIKGALVMPMLIQGYKKGLIKFSIITCR
SEQ ID NO:28  DWSRFVAPFWPAAVIRSAFTWKGLSSLLSSGQKTIKALAMPLMIEGYKKDLIKFAIITCR
SEQ ID NO:08  DWSRFVAPFWPAAVIRSAFTWKGLSSLLSSGKLGI-----YIAFQKQTPPSSSIATCK
SEQ ID NO:22  DWSENVAPFWPAVKSALTWKGFSTLTTGWKTIRGAMVMPLMIQGYKKGLIKFTIITCR
SEQ ID NO:24  -----
SEQ ID NO:26  DWSENVAPFWPAAVKSALTWKGLTSLRSGWETVRGAMVMPLVIEGYKKGLIKFPITTCR
                                     301      360

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FIGURE 1

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SEQ ID NO:39 KPLV-----
SEQ ID NO:40 KPL-----
SEQ ID NO:38 KPQAIEGEPEEAAPSVE.-
SEQ ID NO:28 K-----PE.-----
SEQ ID NO:08 SYVTDHYFHTR.-----
SEQ ID NO:22 KPGAA-.MA----HAALLHC
SEQ ID NO:24 -----
SEQ ID NO:26 KPETT-----Q.-
                               361      380

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FIGURE 2

SEQ ID NO:41	MPPPTTPAATGAAAATPEHARPH-----RMVRENPRSDRFHTLSFHHVEFWCADAASA	60
SEQ ID NO:43	MGHQNAAVSENQNHDDGAASSPGFKLVGFSEKVRKNPKSKDKFKVKRFHHIEFWCGDATNV	
SEQ ID NO:42	MGKKQSEAEILSS-NSSNTSPATFKLVGFNNFVRANPKSDHFAVKRFHHIEFWCGDATNT	
SEQ ID NO:36	MPIPMCNEIQAQA-QAQAQAQPGFKLVGFKNFVRTNPKSDRFQVNRHHIEFWCTDATNA	
SEQ ID NO:38	MPPPTTPAATGAAA-VTPEHARPR-----RMVRENPRSDRFHTLAFHHVEFWCADAASA	
SEQ ID NO:32	MGK-QTTTSATAA-DGSKDAHAEEFKLVGFKNFVRTNPKSDHFCVHREHHIEFWCGDATNT	1
		60
SEQ ID NO:41	AGRFAFALGAPLAARSDLSTGNSAHASQLLRSGSLAFLFTAPYANG-----CDAATASL	
SEQ ID NO:43	ARRFSWGLGMRFSAKSDLSTGNMVHASLYLLTSGDLRFLFTAPYSPSLSAGEIKPTTTASI	
SEQ ID NO:42	SRRFSWGLGMPPLVAKSDLSTGNSVHASLYLRSANLSFVFTAPYSPSTTSS-G---SAAI	
SEQ ID NO:36	SRRFSWGLGMPPIVAKSDLSTGNQIHASLYLLRSGDLSELFSAFYSPSLSAGS-SAASSASI	
SEQ ID NO:38	AGRFAFALGAPLAARSDLSTGNSVHASQLLRSGNLAFLLFTAPYANG-----CDAATASL	
SEQ ID NO:32	AKRFSWGLGMPPLVAKSDLSTGNSAHASLYLLRSGELNFLTSPYSPSISAPS-----SAAI	61
		120
SEQ ID NO:41	PSFSADAARRFSADHGI AVRSV ALRVADAAEAFRASRRRGARPAFAPVDLGRGFA-FAEV	
SEQ ID NO:43	PSFDHGSCRSFFSSHGLGVRAVAIEVEDAESAFSISVANGAIPSSPPIVLNEAVT-IAEV	
SEQ ID NO:42	PSFSASGFHSFAAKHGLAVRAIALEVDVAAAFEAASVARGARPAAPVEL-DDQAWLAEV	
SEQ ID NO:36	PSFDAATCLAFAAKHGFGVRAIALEVDADAEAFSASVAKGAEPASPPV-LVDDRTGFAEV	
SEQ ID NO:38	PSFSADAARQFSADHGLAVRSIALRVADAAEAFRASVDGGARPAFSPVDLGRGFG-FAEV	
SEQ ID NO:32	PSFSFSTYQSFSTSSHGLAVRAVAIQVDSAFSAYSASISRGAKPVSAPIILLSDNKTAIAEV	121
		180

## FIGURE 2

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SEQ ID NO:41  ELYGDEVVLRVFSH-PDGTDP-----FLPGFEGVTNPD-----VDYGLTRFDHVVGNNVP
SEQ ID NO:43  KLYGDEVVLRVVSYKAEDTEKSE-----FLPGFERVEDASSFP-LDYGIRRLDHAAGNNVP
SEQ ID NO:42  ELYGDEVVLRVFSFGRE-----EGLFLPGFEAVEGTASFPDLDYGIRRLDHAAGNNVT
SEQ ID NO:36  RLYGDEVVLRVVSYKDAAPQAPHADPSRWFLPGFEAAASSSFPELDYGIRRLDHAAGNNVP
SEQ ID NO:38  ELYGDEVVLRVFSH-PDGRDVP-----FLPGFEGVSNPD-----VDYGLTRFDHVVGNNVP
SEQ ID NO:32  HLYGDSVLRVFSYGDNG-----TGPDCWFLPGFEPVDDQMSYKELDYGIRRLDHAAGNNVP
                                     181
                                     240

SEQ ID NO:41  ELAPAAAYIAGFTGFHFAEFTAEADVGTESGLNSVVLANNSEGVLLPLNEPVHGTKRRS
SEQ ID NO:43  ELGPALTYVAGFTGFHQFAEFTADDDVGTAEGLNSAVLASNDEMVLPLINEPVHGTKRKS
SEQ ID NO:42  ELGPVVEYIKGFTGFHFAEFTAEADVGTESGLNSVVLANNSEMVLLPLNEPVYGTKRKS
SEQ ID NO:36  ELAPAVRYLKGFSGFHFAEFTAEADVGTESGLNSVVLANNSETVLLPLNEPVYGTKRKS
SEQ ID NO:38  ELAPAAAYVAGFTGFHFAEFTTEDVGTAEGLNSMVLANNSEGVLLPLNEPVHGTKRRS
SEQ ID NO:32  ELGPVVDYLLKFTGFHFAEFTSEDVGTAEGLNSMVLANNSENVLLPLNEPVFGTKRKS
                                     241
                                     300

SEQ ID NO:41  QIQTFLEHHGGPGVQVQHIAVASSDVLRTLRKMRRARSAMGGDFLPPPLPKYYEGVRRRIAGD
SEQ ID NO:43  QIQTYLEHNEGAGLQHLALMSEDI FRTLREMRKRSSIGGDFMPSPPPTYYQNLKRVGD
SEQ ID NO:42  QIQTYLEHNEGAGVQHLALVSEDI FRTLREMRKRSCLGGEFMPSPPTYYKLNKRVGD
SEQ ID NO:36  QIETYLEHNEGAGVQHLALVTHDI FTTLREMRKRSSFLLGGFEFMPSPPTYYANLHNRAAD
SEQ ID NO:38  QIQTFLEHHGGSGVQVQHIAVASSDVLRTLREMRARSAMGGDFLPPPLPKYYEGVRRRIAGD
SEQ ID NO:32  QIQTYLEHNEGPGVQVQHLALVSEDI FNTLREMRKRSGVGGFEFMPSPPLTYKLNKVRAGD
                                     301
                                     360

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# FIGURE 2

SEQ ID NO: 41	VLSEAQIKECQELGVLVDRDDQGVLLQIFTKPVGDRPTLFLEMIQRIIGCMKDERGEEYQ	420
SEQ ID NO: 43	VLSDDDQIKECEEELGILVDRDDQGTLLQIFTKPLGDRPTIFIEIIQRVGCMKDEEGKAYQ	
SEQ ID NO: 42	VLSDEQIKECEDLGILVDRDDQGTLLQIFTKPVGDRPTLFIEIIQRVGCMKDDAGQMYQ	
SEQ ID NO: 36	VLTVDDQIKQCEEELGILVDRDDQGTLLQIFTKPVGDRPTIFIEIIQRIIGCMVEDEEGKVYQ	
SEQ ID NO: 38	VLSEAQIKECQELGVLVDRDDQGVLLQIFTKPVGDRPTLFLEMIQRIIGCMKDERGEEYQ	
SEQ ID NO: 32	VLRDEQIEECEEKLGILVDRDDQGTLLQIFTKPVGDRPTLFIEIIQRIIGCMKDEQKLYQ	361
SEQ ID NO: 41	KGCGGGFGKGNFSELFKSIEDYEKSLEAKQSAAVQG-S	
SEQ ID NO: 43	SGCGGGFGKGNFSELFKSIEEYEKTLQAKQLVG-----	
SEQ ID NO: 42	KGCGGGFGKGNFSELFKSIEEYEKTLQAKQITGSA-AA	
SEQ ID NO: 36	KGACGGFGKGNFSELFKSIEEYEKTLQAKR-----TA.	
SEQ ID NO: 38	KGCGGGFGKGNFSELFKSIEDYEKSLEAKQSAAVQGS.	
SEQ ID NO: 32	KSGCGGGFGKGNFSELFKSIEEYEKMLEAKQVTTETASA.	421

Figure 3

